



## SEQUENCE LISTING

<110> Hitz, William  
Sebastian, Scott  
Grace, John  
Streit, Leon

<120> SOYBEAN PLANT PRODUCING SEEDS WITH REDUCED LEVELS OF RAFFINOSE  
SACCHARIDES AND PHYTIC ACID

<130> BB-1077-C

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<150> 08/835,751

<151> APRIL 8, 1997

<150> PCT/US98/06822

<151> APRIL 7, 1998

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<170> Microsoft Office 97

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<212> DNA

<213> Glycine max

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His	Glu	Asn	Arg	Asn	Gly	Thr	Tyr	Gln	Trp	Ile	Val	Lys	Pro	Lys	Ser	
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Val	Lys	Tyr	Glu	Phe	Lys	Thr	Asn	Ile	His	Val	Pro	Lys	Leu	Gly	Val	
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Gln	Gln	Ala	Asn	Tyr	Phe	Gly	Ser	Leu	Thr	Gln	Ala	Ser	Ala	Ile	Arg	
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Val	Ile	Lys	Tyr	Val	Pro	Tyr	Val	Gly	Asp	Ser	Lys	Arg	Ala	Met	Asp
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His	Asn	Thr	Cys	Glu	Asp	Ser	Leu	Leu	Ala	Ala	Pro	Ile	Ile	Leu	Asp
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 <212> DNA  
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<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

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<211> 1533

<212> DNA

<213> Glycine max

<400> 5

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<212> PRT

<213> Glycine max

<400> 6

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Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
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His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
      35             40             45

Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val
      50             55             60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
      65             70             75             80
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Val	Ile	Ala	Asn	Arg	Glu	Gly	Ile	Ser	Trp	Ala	Thr	Lys	Asp	Lys	Ile	85	90	95
Gln	Gln	Ala	Asn	Tyr	Phe	Gly	Ser	Leu	Thr	Gln	Ala	Ser	Ala	Ile	Arg	100	105	110
Val	Gly	Ser	Phe	Gln	Gly	Glu	Glu	Ile	Tyr	Ala	Pro	Phe	Lys	Ser	Leu	115	120	125
Leu	Pro	Met	Val	Asn	Pro	Asp	Asp	Ile	Val	Phe	Gly	Gly	Trp	Asp	Ile	130	135	140
Ser	Asn	Met	Asn	Leu	Ala	Asp	Ala	Met	Ala	Arg	Ala	Lys	Val	Phe	Asp	145	150	155
Ile	Asp	Leu	Gln	Lys	Gln	Leu	Arg	Pro	Tyr	Met	Glu	Ser	Met	Leu	Pro	165	170	175
Leu	Pro	Gly	Ile	Tyr	Asp	Pro	Asp	Phe	Ile	Ala	Ala	Asn	Gln	Glu	Glu	180	185	190
Arg	Ala	Asn	Asn	Val	Ile	Lys	Gly	Thr	Lys	Gln	Glu	Gln	Val	Gln	Gln	195	200	205
Ile	Ile	Lys	Asp	Ile	Lys	Ala	Phe	Lys	Glu	Ala	Thr	Lys	Val	Asp	Lys	210	215	220
Val	Val	Val	Leu	Trp	Thr	Ala	Asn	Thr	Glu	Arg	Tyr	Ser	Asn	Leu	Val	225	230	235
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Asn	Glu	Ala	Glu	Ile	Ser	Pro	Ser	Thr	Leu	Tyr	Ala	Ile	Ala	Cys	Val	260	265	270
Met	Glu	Asn	Val	Pro	Phe	Ile	Asn	Gly	Ser	Pro	Gln	Asn	Thr	Phe	Val	275	280	285
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Phe	Leu	Val	Gly	Ala	Gly	Ile	Lys	Pro	Thr	Ser	Ile	Val	Ser	Tyr	Asn	325	330	335
His	Leu	Gly	Asn	Asn	Asp	Gly	Met	Asn	Leu	Ser	Ala	Pro	Gln	Thr	Phe	340	345	350
Arg	Ser	Lys	Glu	Ile	Ser	Lys	Ser	Asn	Val	Val	Asp	Asp	Met	Val	Asn	355	360	365
Ser	Asn	Ala	Ile	Leu	Tyr	Glu	Pro	Gly	Glu	His	Pro	Asp	His	Val	Val	370	375	380
Val	Ile	Lys	Tyr	Val	Pro	Tyr	Val	Gly	Asp	Ser	Asn	Arg	Ala	Met	Asp	385	390	395
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 His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp  
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 435 440 445  
 Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser  
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 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn  
 465 470 475 480  
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<210> 7  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 7  
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<210> 8  
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<220>  
 <223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 8  
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<210> 9  
 <211> 1533  
 <212> DNA  
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<211> 510

<212> PRT

<213> Glycine max

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          20                      25                      30

```

```

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
          35                      40                      45

```

```

Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val
          50                      55                      60

```

```

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
          65                      70                      75                      80

```

```

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
          85                      90                      95

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Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
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```

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
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Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
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```

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Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
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```

```

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro
          165                      170                      175

```

```

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
          180                      185                      190

```

```

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
          195                      200                      205

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225					230					235					240		
Val	Gly	Leu	Asn	Asp	Thr	Met	Glu	Asn	Leu	Leu	Ala	Ala	Val	Asp	Arg		
				245					250					255			
Asn	Glu	Ala	Glu	Ile	Ser	Pro	Ser	Thr	Leu	Tyr	Ala	Ile	Ala	Cys	Val		
			260					265						270			
Met	Glu	Asn	Val	Pro	Phe	Ile	Asn	Gly	Ser	Pro	Gln	Asn	Thr	Phe	Val		
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Asp	Asp	Phe	Lys	Ser	Gly	Gln	Thr	Lys	Met	Lys	Ser	Val	Leu	Val	Asp		
305					310					315					320		
Phe	Leu	Val	Gly	Ala	Gly	Ile	Lys	Pro	Thr	Ser	Ile	Val	Ser	Tyr	Asn		
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His	Leu	Gly	Asn	Asn	Asp	Gly	Met	Asn	Leu	Ser	Ala	Pro	Gln	Thr	Phe		
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Val	Gly	Leu	Ala	Pro	Glu	Asn	Asn	Met	Ile	Leu	Glu	Tyr	Lys				
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<210> 11

<211> 1533



<212> DNA

<213> Glycine max

<400> 11

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cagtggattg tcaaacccaa atccgtcaac taccaattta aaaccaacac ccatgttcca 180
aaattggggg tgatgcttgt ggggtggggg ggaaacaacg gctctaccct caccggtggg 240
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tactttggct ccctcaccca agcctcagct attcgagttg gatccttcca gggagaggaa 360
atctatgccc cattcaagag tctgcttcca atggttaatc ctgacgacat tgtgtttggg 420
ggatgggata tcagcaacat gaacctggct gatgccatgg ccagggcaaa ggtgtttgac 480
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tacgacccgg atttcattgc tgccaacca gaggagcgtg ccaacaacgt gattaagggc 600
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aaagtggaca aggtggttgt cctgtggact gccaacacag agaggtatag caatttgggt 720
gtaggcctta atgacaccat ggagaatctc ttggctgctg tggacagaaa tgaggctgag 780
atttctcctt ccaccttgta tgccattgcc tgtgtgatgg aaaatgttcc tttcattaat 840
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ttgattgggt gagatgactt caagagtggg cagaccaaaa tgaaatctgt gttggttgat 960
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aacgttgttg acgatatggt caacagcaat gccatcctct atgagcctgg tgaacatccc 1140
gaccatgttg ttgttattaa gtatgtgcct tacgtagggg atagcaagag agccatggat 1200
gagtacactt cagagatatt catgggtgga aagaacacca ttgttttgca caacacatgt 1260
gaggattccc ttttagctgc tcctattatc ttggacttgg tccttcttgc tgagctgagc 1320
actagaatcc agtttaaagc tgaaaatgag ggaatttcc actcattcca cccagttgct 1380
accattctca gctatctgac caaggctcct ctggttccac cgggtacacc agtgggtgaat 1440
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ccagagaata acatgattct cgagtacaag tga 1533
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<210> 12

<211> 510

<212> PRT

<213> Glycine max

<400> 12

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Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
      20                      25                      30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
      35                      40                      45

Val Asn Tyr Gln Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val
      50                      55                      60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
      65                      70                      75                      80

Val Ile Ala Asn Arg Glu Asp Ile Ser Trp Ala Thr Lys Asp Lys Ile
      85                      90                      95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
      100                      105                      110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
      115                      120                      125
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Leu	Pro	Met	Val	Asn	Pro	Asp	Asp	Ile	Val	Phe	Gly	Gly	Trp	Asp	Ile	
	130					135					140					
Ser	Asn	Met	Asn	Leu	Ala	Asp	Ala	Met	Ala	Arg	Ala	Lys	Val	Phe	Asp	
145					150					155					160	
Ile	Asp	Leu	Gln	Lys	Gln	Leu	Arg	Pro	Tyr	Met	Glu	Ser	Met	Val	Pro	
				165					170					175		
Leu	Pro	Gly	Ile	Tyr	Asp	Pro	Asp	Phe	Ile	Ala	Ala	Asn	Gln	Glu	Glu	
			180					185					190			
Arg	Ala	Asn	Asn	Val	Ile	Lys	Gly	Thr	Lys	Gln	Glu	Gln	Val	Gln	Gln	
		195					200					205				
Ile	Ile	Lys	Asp	Ile	Lys	Ala	Phe	Lys	Glu	Ala	Thr	Lys	Val	Asp	Lys	
	210					215					220					
Val	Val	Val	Leu	Trp	Thr	Ala	Asn	Thr	Glu	Arg	Tyr	Ser	Asn	Leu	Val	
225					230					235					240	
Val	Gly	Leu	Asn	Asp	Thr	Met	Glu	Asn	Leu	Leu	Ala	Ala	Val	Asp	Arg	
				245					250					255		
Asn	Glu	Ala	Glu	Ile	Ser	Pro	Ser	Thr	Leu	Tyr	Ala	Ile	Ala	Cys	Val	
			260					265					270			
Met	Glu	Asn	Val	Pro	Phe	Ile	Asn	Gly	Ser	Pro	Gln	Asn	Thr	Phe	Val	
		275					280					285				
Pro	Gly	Leu	Ile	Asp	Leu	Ala	Ile	Ala	Arg	Asn	Thr	Leu	Ile	Gly	Gly	
	290					295					300					
Asp	Asp	Phe	Lys	Ser	Gly	Gln	Thr	Lys	Met	Lys	Ser	Val	Leu	Val	Asp	
305					310					315					320	
Phe	Leu	Val	Gly	Ala	Gly	Ile	Lys	Pro	Thr	Ser	Ile	Val	Ser	Tyr	Asn	
				325					330					335		
His	Leu	Gly	Asn	Asn	Asp	Gly	Met	Asn	Leu	Ser	Ala	Pro	Gln	Thr	Phe	
			340					345					350			
Arg	Ser	Lys	Glu	Ile	Ser	Lys	Ser	Asn	Val	Val	Asp	Asp	Met	Val	Asn	
		355					360					365				
Ser	Asn	Ala	Ile	Leu	Tyr	Glu	Pro	Gly	Glu	His	Pro	Asp	His	Val	Val	
	370					375					380					
Val	Ile	Lys	Tyr	Val	Pro	Tyr	Val	Gly	Asp	Ser	Lys	Arg	Ala	Met	Asp	
385					390					395					400	
Glu	Tyr	Thr	Ser	Glu	Ile	Phe	Met	Gly	Gly	Lys	Asn	Thr	Ile	Val	Leu	
				405					410					415		
His	Asn	Thr	Cys	Glu	Asp	Ser	Leu	Leu	Ala	Ala	Pro	Ile	Ile	Leu	Asp	
			420					425					430			
Leu	Val	Leu	Leu	Ala	Glu	Leu	Ser	Thr	Arg	Ile	Gln	Phe	Lys	Ala	Glu	
		435					440					445				

Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser  
 450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn  
 465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys  
 485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys  
 500 505 510

<210> 13  
 <211> 1533  
 <212> DNA  
 <213> Glycine max

<400> 13  
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 cagtcctgtg acaactacga aaccaccgaa cttgttcacg agaacaggaa tggcacctat 120  
 cagtggattg tcaaacccaa atcctgcaac taccaattta aaaccaacac ccatgttcca 180  
 aaattggggg tgatgcttgt ggggtggggg ggaacaacg gctctaccct caccgggtgt 240  
 gttattgcta acagagaggg catttcatgg gctacaaagg acaagattca acaagccaat 300  
 tactttggct ccctcaccca agcctcagct attcgagttg gatccttcca gggagaggaa 360  
 atctatgccc cattcaagag totgcttcca atgggttaatc ctgacgacat tgtgtttggg 420  
 ggatgggata tcagcaacat gaacctggct gatgccatgg ccagggcaaa ggtgtttgac 480  
 atcgatttgc agaagcagtt gaggccttac atggaatcca tggttccact ccccggaatc 540  
 tacgaccggg atttcattgc tgccaaccaa gaggagcgtg ccaacaacgt gattaagggc 600  
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 aaagtggaca aggtggttgt cctgtggact gccaacacag agaggtatag caatttggtt 720  
 gtaggcctta atgacaccat ggagaatctc ttggctgctg tggacagaaa tgaggctgag 780  
 atttctcctt ccaccttgta tgccattgcc tgtgtgatgg aaaatgttcc ttctattaat 840  
 ggaagccctc agaacacttt tgtaccaggg ctgattgatc ttgccatcgc gaggaacact 900  
 ttgattgggt gagatgactt caagagtggg cagacccaaa tgaaatctgt gttggttgat 960  
 tttcttggtg gggctggtat caagccaaca tctatagtta gttacaacca tctgggaaac 1020  
 aatgatggta tgaatctctc ggctccacaa accttccgt ccaaggaaat ctccaagagc 1080  
 aacgttggtg acgatatggt caacagcaat gccatcctct atgagcctgg tgaacatccc 1140  
 gacctgttg ttgttattaa gtatgtgcct tacgtagggg atagcaagag agccatggat 1200  
 gactacactt cagagatatt catgggtgga aagaacacca ttgttttgca caacacatgt 1260  
 gaggattccc ttttagctgc tcctattatc ttggacttgg tccttcttgc tgagctgagc 1320  
 actagaatcc agtttaaagc tgaaaatgag ggaaaattcc actcattcca cccagttgct 1380  
 accattctca gctatctgac caaggctcct ctggttccac cgggtacacc agtgggtgaat 1440  
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 ccagagaata acatgattct cgagtacaag tga 1533

<210> 14  
 <211> 510  
 <212> PRT  
 <213> Glycine max

<400> 14  
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 Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val  
 20 25 30  
 His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser  
 35 40 45

Val	Asn	Tyr	Gln	Phe	Lys	Thr	Asn	Thr	His	Val	Pro	Lys	Leu	Gly	Val	50	55	60	
Met	Leu	Val	Gly	Trp	Gly	Gly	Asn	Asn	Gly	Ser	Thr	Leu	Thr	Gly	Gly	65	70	75	80
Val	Ile	Ala	Asn	Arg	Glu	Gly	Ile	Ser	Trp	Ala	Thr	Lys	Asp	Lys	Ile	85	90	95	
Gln	Gln	Ala	Asn	Tyr	Phe	Gly	Ser	Leu	Thr	Gln	Ala	Ser	Ala	Ile	Arg	100	105	110	
Val	Gly	Ser	Phe	Gln	Gly	Glu	Glu	Ile	Tyr	Ala	Pro	Phe	Lys	Ser	Leu	115	120	125	
Leu	Pro	Met	Val	Asn	Pro	Asp	Asp	Ile	Val	Phe	Gly	Gly	Trp	Asp	Ile	130	135	140	
Ser	Asn	Met	Asn	Leu	Ala	Asp	Ala	Met	Ala	Arg	Ala	Lys	Val	Phe	Asp	145	150	155	160
Ile	Asp	Leu	Gln	Lys	Gln	Leu	Arg	Pro	Tyr	Met	Glu	Ser	Met	Val	Pro	165	170	175	
Leu	Pro	Gly	Ile	Tyr	Asp	Pro	Asp	Phe	Ile	Ala	Ala	Asn	Gln	Glu	Glu	180	185	190	
Arg	Ala	Asn	Asn	Val	Ile	Lys	Gly	Thr	Lys	Gln	Glu	Gln	Val	Gln	Gln	195	200	205	
Ile	Ile	Lys	Asp	Ile	Lys	Ala	Phe	Lys	Glu	Ala	Thr	Lys	Val	Asp	Lys	210	215	220	
Val	Val	Val	Leu	Trp	Thr	Ala	Asn	Thr	Glu	Arg	Tyr	Ser	Asn	Leu	Val	225	230	235	240
Val	Gly	Leu	Asn	Asp	Thr	Met	Glu	Asn	Leu	Leu	Ala	Ala	Val	Asp	Arg	245	250	255	
Asn	Glu	Ala	Glu	Ile	Ser	Pro	Ser	Thr	Leu	Tyr	Ala	Ile	Ala	Cys	Val	260	265	270	
Met	Glu	Asn	Val	Pro	Phe	Ile	Asn	Gly	Ser	Pro	Gln	Asn	Thr	Phe	Val	275	280	285	
Pro	Gly	Leu	Ile	Asp	Leu	Ala	Ile	Ala	Arg	Asn	Thr	Leu	Ile	Gly	Gly	290	295	300	
Asp	Asp	Phe	Lys	Ser	Gly	Gln	Thr	Lys	Met	Lys	Ser	Val	Leu	Val	Asp	305	310	315	320
Phe	Leu	Val	Gly	Ala	Gly	Ile	Lys	Pro	Thr	Ser	Ile	Val	Ser	Tyr	Asn	325	330	335	
His	Leu	Gly	Asn	Asn	Asp	Gly	Met	Asn	Leu	Ser	Ala	Pro	Gln	Thr	Phe	340	345	350	
Arg	Ser	Lys	Glu	Ile	Ser	Lys	Ser	Asn	Val	Val	Asp	Asp	Met	Val	Asn	355	360	365	

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val  
 370 375 380  
 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp  
 385 390 395 400  
 Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu  
 405 410 415  
 His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp  
 420 425 430  
 Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu  
 435 440 445  
 Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser  
 450 455 460  
 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn  
 465 470 475 480  
 Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys  
 485 490 495  
 Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys  
 500 505 510

<210> 15  
 <211> 1533  
 <212> DNA  
 <213> Glycine max

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 cagtggattg tcaaacccaa atccgtcaac taccaattta aaaccaacac ccatgttcca 180  
 aaattggggg tgatgcttgt ggggttggggg ggaacaacg gctctaccct caccggtggt 240  
 gttattgcta acagagaggg catttcacgg gctacaaagg acaagattca acaagccaat 300  
 tactttggct ccctcaccca agcctcagct attcgagttg gatccttcca gggagaggaa 360  
 atctatgccc cattcaagag tctgcttcca atgggttaatc ctgacgacat tgtgtttggg 420  
 ggatgggata tcagcaacat gaacctggct gatgccatgg ccaggggcaaa ggtgtttgac 480  
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 tacgaccggg atttcattgc tgccaacca gaggagcgtg ccaacaacgt gattaagggc 600  
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 gtaggcctta atgacacat ggagaatctc ttggctgctg tggacagaaa tgaggctgag 780  
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 aatgatggta tgaatctctc ggctccaca accttccgct ccaaggaaat ctccaagagc 1080  
 aacgttgttg acgatattgt caacagcaat gccactctct atgagcctgg tgaacatccc 1140  
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 gagtacactt cagagatatt catgggtgga aagaacacca ttgttttgca caacacatgt 1260  
 gaggattccc ttttagctgc tcctattatc ttggacttgg tccttcttgc tgagctgagc 1320  
 actagaatcc agtttaaagc tgaaaatgag ggaaaattcc actcattcca cccagttgct 1380  
 accattctca gctatctgac caaggctcct ctggttccac cgggtacacc agtggtgaat 1440  
 gcattgtcaa agcagcgtgc aatgctggaa aacataatga gggcttgtgt tggattggcc 1500  
 ccagagaata acatgattct cgagtacaag tga 1533

<210> 16  
<211> 510  
<212> PRT  
<213> Glycine max

<400> 16

Met	Phe	Ile	Glu	Asn	Phe	Lys	Val	Glu	Ser	Pro	Asn	Val	Lys	Tyr	Thr
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Glu	Thr	Glu	Ile	Gln	Ser	Val	Tyr	Asn	Tyr	Glu	Thr	Thr	Glu	Leu	Val
			20					25					30		
His	Glu	Asn	Arg	Asn	Gly	Thr	Tyr	Gln	Trp	Ile	Val	Lys	Pro	Lys	Ser
		35					40					45			
Val	Asn	Tyr	Gln	Phe	Lys	Thr	Asn	Thr	His	Val	Pro	Lys	Leu	Gly	Val
	50					55					60				
Met	Leu	Val	Gly	Trp	Gly	Gly	Asn	Asn	Gly	Ser	Thr	Leu	Thr	Gly	Gly
65					70					75					80
Val	Ile	Ala	Asn	Arg	Glu	Gly	Ile	Ser	Trp	Ala	Thr	Lys	Asp	Lys	Ile
				85					90					95	
Gln	Gln	Ala	Asn	Tyr	Phe	Gly	Ser	Leu	Thr	Gln	Ala	Ser	Ala	Ile	Arg
			100					105					110		
Val	Gly	Ser	Phe	Gln	Gly	Glu	Glu	Ile	Tyr	Ala	Pro	Phe	Lys	Ser	Leu
		115					120					125			
Leu	Pro	Met	Val	Asn	Pro	Asp	Asp	Ile	Val	Phe	Gly	Gly	Trp	Asp	Ile
	130					135					140				
Ser	Asn	Met	Asn	Leu	Ala	Asp	Ala	Met	Ala	Arg	Ala	Lys	Val	Phe	Asp
145					150					155					160
Ile	Asp	Leu	Gln	Lys	Gln	Leu	Arg	Pro	Tyr	Met	Glu	Ser	Met	Val	Pro
				165					170					175	
Leu	Pro	Gly	Ile	Tyr	Asp	Pro	Asp	Phe	Ile	Ala	Ala	Asn	Gln	Glu	Glu
			180					185					190		
Arg	Ala	Asn	Asn	Val	Ile	Lys	Gly	Thr	Lys	Gln	Glu	Gln	Val	Gln	Gln
		195					200					205			
Ile	Ile	Lys	Asp	Ile	Lys	Ala	Phe	Lys	Glu	Ala	Thr	Lys	Val	Asp	Lys
	210					215					220				
Val	Val	Val	Leu	Trp	Thr	Ala	Asn	Thr	Glu	Arg	Tyr	Ser	Asn	Leu	Val
225					230					235					240
Val	Gly	Leu	Asn	Asp	Thr	Met	Glu	Asn	Leu	Leu	Ala	Ala	Val	Asp	Arg
			245					250						255	
Asn	Glu	Ala	Glu	Ile	Ser	Pro	Ser	Thr	Leu	Tyr	Ala	Ile	Ala	Cys	Val
			260					265					270		
Met	Glu	Asn	Val	Pro	Phe	Ile	Asn	Gly	Ser	Pro	Gln	Asn	Thr	Phe	Val
		275					280					285			

Pro	Gly	Leu	Ile	Asp	Leu	Ala	Ile	Ala	Arg	Asn	Thr	Leu	Ile	Gly	Gly	290	295	300	
Asp	Asp	Phe	Lys	Ser	Gly	Gln	Thr	Lys	Met	Lys	Ser	Val	Leu	Val	Asp	305	310	315	320
Phe	Leu	Val	Gly	Ala	Gly	Ile	Lys	Pro	Thr	Ser	Ile	Val	Ser	Tyr	Asn	325	330	335	
His	Leu	Gly	Asn	Asn	Asp	Gly	Met	Asn	Leu	Ser	Ala	Pro	Gln	Thr	Phe	340	345	350	
Arg	Ser	Lys	Glu	Ile	Ser	Lys	Ser	Asn	Val	Val	Asp	Asp	Met	Val	Asn	355	360	365	
Ser	Asn	Ala	Ile	Leu	Tyr	Glu	Pro	Gly	Glu	His	Pro	Asp	His	Val	Val	370	375	380	
Val	Ile	Lys	Tyr	Val	Pro	Tyr	Val	Gly	Asp	Ser	Lys	Arg	Ala	Met	Asp	385	390	395	400
Glu	Tyr	Thr	Ser	Glu	Ile	Phe	Met	Gly	Gly	Lys	Asn	Thr	Ile	Val	Leu	405	410	415	
His	Asn	Thr	Cys	Glu	Asp	Ser	Leu	Leu	Ala	Ala	Pro	Ile	Ile	Leu	Asp	420	425	430	
Leu	Val	Leu	Leu	Ala	Glu	Leu	Ser	Thr	Arg	Ile	Gln	Phe	Lys	Ala	Glu	435	440	445	
Asn	Glu	Gly	Lys	Phe	His	Ser	Phe	His	Pro	Val	Ala	Thr	Ile	Leu	Ser	450	455	460	
Tyr	Leu	Thr	Lys	Ala	Pro	Leu	Val	Pro	Pro	Gly	Thr	Pro	Val	Val	Asn	465	470	475	480
Ala	Leu	Ser	Lys	Gln	Arg	Ala	Met	Leu	Glu	Asn	Ile	Met	Arg	Ala	Cys	485	490	495	
Val	Gly	Leu	Ala	Pro	Glu	Asn	Asn	Met	Ile	Leu	Glu	Tyr	Lys			500	505	510	